

SUMMARIES									
Result No.	Score	Query Length	DB ID	Description					
1	469.8	21.0	807	13	B1764263	807 bp mRNA	linear EST 25-SEP-2001		
2	456.6	20.5	469	10	AV715904	Homo sapiens cDNA clone IMAGE:5186388 5 ,			
c	3	442.8	19.8	457	9	AA694175	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
c	5	422.4	18.9	563	9	AA034153	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
c	6	394.8	17.7	398	9	AA887940	Unpublished (1999)		
c	390.2	17.5	407	14	BQ027284	Contact: Robert Strausberg, Ph.D.			
						Email: cgsbs-f@mail.nih.gov			
						Tissue Procurement: Life Technologies, Inc.			
						CDNA Library Preparation: Life Technologies, Inc.			
						CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
						DNA Sequencing by: Incyte Genomics, Inc.			
						Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:			
						http://image.llnl.gov			
						Plate: LLM11465 row: i column: 13			
						High quality sequence stop: 805.			
						Location/Qualifiers 1. .807			
						FEATURES source			

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:21:24 ; Search time 2812.92 Seconds

(without alignments)
12850.800 Million cell updates/sec

Title: US-09-625-573-1

Sequence: 1 GGATGAAAGGACCGATT.....TATAACTATGGATAAAG 2232

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_sts3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_plan:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_name:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*
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RESULT 1
B1764263
LOCUS 603045953F1 NIH_MGC_116 Homo sapiens mRNA
DEFINITION mRNA sequence.

ACCESSION B1764263
VERSION B1764263.1
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-IGC http://mgc.ncbi.nlm.nih.gov/
AUTHORS /
TITLE /
JOURNAL /
COMMENT 1. (bases 1 to 807)

Tissue Procurement: Life Technologies, Inc.
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11465 row: i column: 13
High quality sequence stop: 805.
Location/Qualifiers 1. .807

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Score	Match	Length	DB ID	Description
469.8	21.0	807	13	B1764263
456.6	20.5	469	10	AV715904
394.8	17.7	398	9	AA887940
390.2	17.5	407	14	BQ027284

Score	Match	Length	DB ID	Description
442.8	19.8	457	9	AA694175
422.4	18.9	563	9	AA034153
394.8	17.7	398	9	AA887940

Mon Jun 2 09:42:08 2003

QY	1655	GCTGTGATCTCAGTGGATCTCCATTCTCTCAAGCTTGGTGCC	1697	Db	338	CCCTGAAGTAAGCAAAGACTTTCCCTTAGTCAGGCCAAGTTAGAAAGTGTCTATGTTG	279
LOCUS	AA694175	457 bp	mRNA	EST	16-DEC-1997	QY	1950
DEFINITION	z142a0.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:43342 3', mRNA sequence.					CCAGTGTGTTCTGATGTGCTATGGCTACATGGCTAAAGAAG 2069	
ACCESSION	AA694175					TGGGAACCTAGACTCCCAAAGCTGGACTATGGCTACATGGCTACATGGCTAAAGAAG 2069	
KEYWORDS	AA694175.1	GI:2695113				QY	2010
ORGANISM	Human					TGGGAACCTAGACTCCCAAAGCTGGACTATGGCTACATGGCTAAAGAAG 159	
MAMMALIA: Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 457)	Hillier,L., Allen,M., Bowles,L., Dubuge,T., Geisel,G., Jost,S., Krizman D., Kucaba,T., Lacy,M., Le,N., Lenion,G., Marra,M., Martin,J., Moore,B., Schellerberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.					GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 2129	
REFERENCE						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 2129	
AUTHORS						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
COMMENT						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
TITLE						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
JOURNAL						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
COMMENT						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
FEATURES source						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
Best Local Similarity 99.3%; Pred. No. 6.3e-104; Matches 455; Conservative 0; Mismatches 2;	Indels 1; Gaps 1;					GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
BASE COUNT ORIGIN	137 a 96 c	82 g 142 t				GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
Query Match Score 442.8; DB 9; Length 457;						GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
Best Local Similarity 99.3%; Pred. No. 6.3e-104; Matches 455; Conservative 0; Mismatches 2;	Indels 1; Gaps 1;					GTTCAGAAAAGAATGGGGCACAGGCAGACTTCACCTCATATTTGATGCTCA 99	
QY	1770	TGCGAGATGCCATTCTCATATGGTCCCTTAATGGCTCAAGGGAACTCCAAATCA	1829	Db	457	TGGAGATGCTCTAACTAAAGCTTAAACCTATGGTAAAGAATGGAAGCTGGAGCTCCPANTCA	399
Matches 455; Conservative 0; Mismatches 2;	Indels 1; Gaps 1;					ACTGGCTCTAACTAAACCTTAAACCTTAAACCTTAAAGAATGGAAGCTGGAGCTCCPANTCA	399
QY	1830	AATTGGCTCTAACTAAAGCTTAAACCTATGGTAAAGAATGGAAGCTGGAGCT 1889		Db	398	AATTGGCTCTAACTAAACCTTAAACCTTAAACCTTAAAGAATGGAAGCTGGAGCT 339	
Db	398	AATTGGCTCTAACTAAACCTTAAACCTTAAACCTTAAAGAATGGAAGCTGGAGCT 1919		QY	1890	CCCGAAGTAAGCAAAGCTTCCCTTAGTCAGGCCAAGTTAGAAAGTGTCTATGTTG	

(Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Benito Soares and M. Fatima Bonaldo.¹⁰

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found at cgap.nci.nih.gov

LIGIN		Sensu	
Query Match	18.9%	Score 421.4;	DB 9;
Best Local Similarity	92.28%	Pred. No. 2	Length 563;
Matches 519; Conservative	0;	Mismatches 32;	Gaps 7;
		Indels 12;	

found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 385.
Location/Qualifiers
1-200

1395	AACTGCAACTTGTAAATGTGGTAAAGAGTTAGTTTGACTGCTATCATGTCAAACGTGA	1454
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1455	AAATGCGTGTAAATTAGTCACAGAGATAATTCTAGCCTTGACCTTAAGATTGAGCAAGTG	1514
61	AAATGCGTGTAAATTAGTCACAGAGATAATTCTAGCCTTGACCTTAAGATTGAGCAAGTG	120
1515	GTAGTTGGAGACTGTGAGTCACCCAAATAGTGTGATTGGCAGGTTGGAAAGTGTGAGGTG	1574
121	GTAGTTGGAGACTGTGAGTCACCCAAATAGTGTGATTGGCAGGTTGGAAAGTGTGAGGTG	180
1575	TGTGATCTGGGGCACATTGGCCTATGCGATGCACCATTAAGTAATGATGTCGTTGTA	1634

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1. .398
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  /clone="IMAGE:1217995"
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  /sex="male"
  /tissue_type="normal prostate"
  /lab_host="DH10B"
  /note="Organ: prostate; Vector: PT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed w
a Not I - oligo(R) primer. Double-stranded cDNA was
ligated to R1 adaptors (Pharmacia), digested with N
I and cloned into the Not I and Eco RI sites of the
modified pGEMTA vector.

```

AA807940.1 GI:2877346
 EST.
 WORDS
 human.
Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 398)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/cnicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strousberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Pumper-McCormick, M.D., Ph.D.

BQ027284	407 bp	mRNA	EST	27-MAR-20
U1-H-COO-ago-h-07-0-U1.s1	linear	Homo sapiens		
IMAGE_3104867 3', mRNA sequence.		cDNA clone		
BQ027284				
BQ027284.1	GI:19762563			
EST				
human				
Eukaryotes				
Homo sapiens				
Chordata				
Gnathostomata				
Vertebrata				
Mammalia				
Primates				
Hominoidea				
Hominidae				
PanTro2				
2163				

FEATURES	
source	IMAGE Consortium (info@image.llnl.gov) for further information.
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Seq. Primer:	Promega -21ml3
High quality sequence stop:	335.
Location/Qualifiers	
1. .461	
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/db_xref="GDB:3773646"	
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/clone="IMAGE:204515"	
/clone.lib="Soares fetal liver spleen 1NFLS"	
/sex="male"	
/dev_stage="20 week-post conception fetus"	
/lab_host="D10B (ampicillin resistant)"	
/note="Organ: Liver and Spleen; Site: 1; Pac I; Site: 2; EcoR1 with a modified polylinker; Site: 1; Pac I; Site: 2; Oligo(dT) primer strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACUCCAAATTTAAGATCTTTCCTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the PUC18 vector (Pharmacia). The modified PUC18 vector, Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."	
119 a	97 c 144 t 96 g 5 others
BASE COUNT	BRITAIN

Qy 280 CTGGCTCAACCGGCCATCUTGATCUTGCTTTCCTATTACTCTCCCATTTGGGTCAAC 339
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 243 CCTCCCTAACCTGGCCATTCTGACCTTCGCTCCCTGCAGCTTCGATGAC 302
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 340 TCTGCTGCAA -- ATCAGTGGCTTGGGAATGCAATGTCGAATTATTCACAGGGCTG 396
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 303 TACAAGTTGAAGGATRACTGCTTGGTATGGCAATGTTAAGATCTCTGGTT 362
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 397 TATCACATGGTATTGGCGGAATCTCTCATCATGCAATCGATAGATAC 456
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 363 TATTACAGGCTTGACAGGAGATCTTTCATCATCTCTGCTGAGATGACAGTAC 422
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 457 CTGGCTATGTCATGCTGTTGGCTTAAAGCCAGACGGTCACTTGGGTGCTG 516
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 423 CTGGCCATCTGTCACGGTGTGGCTGGGGCACGGACGGTCACTTGGTGCATC 482
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 517 ACAAGTGGATACCTGGTTGGCTGCTGTCAGGAAATCATCTTFACT 576
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 Db 483 ACCAGCATCATATTGGCCCTGGCCATCTGGCTCATGCCAGGCTTATCTTCCC 542
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 Db 543 AAGACCCCATGGAAATTCACTCACCAACCTGAGCTTCACCTTCACCAAGCTA 602
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 Qy 625 CGAGGATGAAATAATTTCACACAAATATGAGAACATTTGGGCCCTGCTG 684
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 Db 603 CGAGAGTGGAAAGCTGGTTCAGGCTCTGAAACCTAACCTCTGGCTGTGCTG 662
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 Qy 685 CTCATCAGTGGTCAATCTGGTAAACCTGCTGAAACCTGCTGGTGGAAACGAG 744
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 Db 663 TTGGTCAGTATCCTGGCTACAGGGATTATAAAGATCTGCTTAAGGACCAAATAG 722
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 Qy 745 AAGAGAGGCATAGGGCAACTGGTCACTTCACCATGATTGTTACTTCTCTTC 804
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 Db 780 TGGACCCCTACNATTGACTATACCTTCAGGATTCGGCTGAGTCTGTCACCCAT 839
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 Db 840 GAGTGTGAGCAGGAGACATTTGGACCTGGCTGTGAAGTGAACGGAACTGATCG 895
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Search completed: June 1, 2003, 20:03:35
 Job time : 2826.92 secs

